

Figure 16: Multiple Sequence Alignments of Mil.1.1, Mil.1.2 and Rpi-blb2 nucleic acids

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: Mil.1 3768 bp
 Sequence 2: Mil.1.2 3774 bp
 Sequence 3: Rpi-blb2 3804 bp
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 95
 Sequences (1:3) Aligned. Score: 89
 Sequences (2:3) Aligned. Score: 89
 Guide tree file created: [/ebi/externserv/clustalw-work/interactive/clustalw-20040503-14435620.dnd]
 Start of Multiple Alignment
 There are 2 groups
 Aligning...
 Group 1: Sequences: 2 Score:68908
 Group 2: Sequences: 3 Score:65855
 Alignment Score 66872
 CLUSTAL-Alignment file created [/ebi/externserv/clustalw-work/interactive/clustalw-20040503-14435620.aln]

CLUSTAL W (1.82) multiple sequence alignment

Mil.1 ATGGAACGAAAGATAATGAAGAAAGCAAACTCATTGGTGCTATTTCTGCTCTT 60
 Mil.1.2 ATGGAACGAAAGATAATGAAGAAAGCAAACTCATTGGTGCTATTTCTGCTCTT 60
 Rpi-blb2 ATGGAACGAAAGATAATGAAGAAAGCAAACTCATTGGAGTCATTTCTGCTCTT 60
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Replacement Sheets

Mi1.1
AGCAAGGACATGCGGATGTTCTGGTTTCTCTAGAGA-----ATGAGGAAATCAA 111

Mi1.2
AGCAAGGACAT^TGCCTCAAT^TCTAA^TTTCTCTAGAGA-----ATGAGGAAATCAA 111

Rpi-blb2
CGCAAGGATGCTGCCAATGTTCTGGATTTCTAGAGAGATTAAAGAATGAAGAAGATCAA 120

Mil.1
AAAGCTCTTGACAAAGATCAAGTGAAGATAAAATTGAAAAATGGCATTATTGTACA 171

Mi1.2
AAAGCTCTTGACAAAGATCAAGTTGAAAAGCTAAAATTGAAAATGGCATTTATTGTACA 171

Rpi-blb2
AAGCCTGTTGATGTGGATCTGATTGAAAGCCCTGAAATTGAAGCTGACATTTATTGTACA 180

[illegible]

Mi1.1
TATGTTCAGCTTTCTTGTTCCGATTTTGAGCAGTTTGAAGATATAATGACTAGAAAAAGA 231

Mi1.2
TATGTTCAGCCTTCTTATTCCGATTTTGAGCAGTTTGAGATATAATGACTAGAAATAGA 231

Rpi-blb2
TATGTCCAGCTTTCCTTATTCCGATTTCGAGAAGTTTGAAGATATAATGACTAGAAAAAGA 240

Mi1.1
CAAGAGGTTGAGAAATCTGCTTCAACCACCTTTTGGATGATGATG----- 274

Mi1.2
CAAGAGGTTGAGAAATCTGCTTCAATCACTTTTGGATGATGATG----- 274

Rpi-blb2
CAAGAGTTGAGAAATCTGCTTCAACCAATTTTGGATGATGATGGCAAGACGTCGGGTGT 300

-----TCTTTACTAGCCTCACCAGTAATATGGATGACTGTATCAGCTTGATCATCGT 327

Mil.2
-----TCCTTACTAGCCTCACCAGTAATATGGATGACTGTATCAGCTTGTATCATTCGT 327

Rpi-blb2
AAATATGTCCTTACTAGCCTCGCCGGTAATATGGATGACTGTATAGCTTGTATCATCGT 360

[illegible]

Mi1.1
TCTTATAAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCCTCCTTGAATCTC 387

Mi1.2
TCTTATAATCAGATGCCATCATGATGGATGAGCAATTGGACTTCTCTCTTGAATCTG 387

Rpi-blb2
TCT---AATCAGATGCCACCATGATGGATGAGCAATTGGGCTTCTCTTGAATCTC 417

[illegible]

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Replacement Sheets

	447	447	477
Mi1.1	TATCATCTATCCAAGCATCAGCTGAAAAGATAATTTCTCGAGTGACTCAATATGAAGTT		
Mi1.2	TATCATCTATCCAAGCATCAGCTGAAAAGATAATTTCTCGAGTGACTCAATATGAAGTT		
Rpi-blb2	TCTCATCTATCCAAGCATCGTGCTGAAAAGATGTTTCTCGAGTGACTCAATATGAAGTT		
	* * * * *	* * * * *	* * * * *

Mil1.1 CTTCAGAAATATGTGGCAACATAAGAGATTTCATGGGTTGATAGTGAATGGTTGCATT 507

Mil1.2 CTTCAGAAATGTATGTGGCAACATAAGAGATTTCATGGGTTGATAGTGAATGGTTGCATT 507

Rpi-blb2 CTTCAGAAATGTATGTGGCAACATAAGAGATTTCATGGATTGATAGTGAATTTGTTGCATT 537

Mil.1
AAGCATGAGATGGTTGAGAAATGTCTTRCCTCTGTTTCAACTCATGGCTGACAGAGTAGGA 567

Mil.2
AAGCATGAGATGGTTGAGAAATGTCTTACCTCTGTTTCAACTCATGGCTGAAAAGAGTAGGA 567

Rpi-blb2
AAGCATGAGATGGTTGAGAAATGTCTTATCTCTGTTTCAACTGATGGCTGAGAGAGTAGGA 597

Mi1.1
 Mi1.2
 Rpi-blb2

Accession	Sequence	Length
Mil.1	GAACAAATGATAGAGACTCTCGACTTTTCAAGCTAGCACATCTACTCTTGAAGATCGTT	687
Mil.2	GAACACAATGATAGAGACTCTCGACTCTTCCAGCTAACACATCTACTCTTGAAGATTGTT	687
Rpi-blb2	GATCAGAATGATAAAGAGACCCCTCAACTCTTCAAGCTAGCACATCTACTCTTGAAGATTGTT	717

Mil.1	CCGGTTGAACTGGAGGTTATACACATATGTTATACAAACTTGAAAAGCTTCAAACCTTCAGCT	747
Mil.2	CAACTGAACTGGAGGTTATGCACATATGTTATACAAATTTGAAAAGCTTCAAACCTTCAGCA	747
Rpi-blb2	CCAACTGAATGGAGGTTATGCACATATGTTATATAAACTTTGAAAAGCTTCAAACCTTCAACA	777

Mil.1
GAAGTTGGACTCTTCATTAAGCAGCTTCTAGAAACCTCTCCAGATATTTCTGAGGGAATAT 807

Mi1.2
Rpi-blb2
GAAGTTGGACGCTTCATTAAAGAAGCTCCTGTGAAACCTCACCGGATATTCTCAGAGAATAT 807
GAAATTGGACGCTTCATTAAAGAAGCTCCTGTGAAACCTCTCCGGACATTCTCAGAGAATAT 837
*** ***** ** ** ***** ** ** ***** ** *****

Mi1.1
Mi1.2
Rpi-blb2
CTAATTCCCTCTGCAAGAGCACATGGTAACCTGTTATTACCCCTAGCACCTTCAGGGGCTCGA 867
ATCATTTCAACTACAAGAGCATATGTTAACTGTTATTCCCCCTAGCACCTTAGGGGCTCGA 867
CTGATTCATCTACAAGAGCATATGATAAAGTGTATTACCCCTAACACTTCAGGGGCTCGA 897
* **** ** ***** ** ** ***** ** ***** *****

Mi1.1
Mi1.2
Rpi-blb2
AACATTTCATGTCATGATGGAAATTCCTATTACTTATTCTTTCTGTATATGCC--CAAGGAC 924
AACATTTCATGTCATGATGGAAATTCCTATTACTTATTCTTTCTGTATATGCC--CAAGGAC 924
AACATTTCATGTCATGATGGAAATTCCTATTGATTATTCTTTCTGTATATGCCGCCCAAGGAC 957
***** ***** ***** ***** *****

Mi1.1
Mi1.2
Rpi-blb2
TTTATTTCATCATGACAAACTTTTGTATCTCTTGGATCGTGTGGAGTACTTACCAGGGAG 984
TTTATTTCATCATGACAAACTTTTGTATCTCTTGGCTCATGTTGGAACACTTACCAGGGAG 984
TTTATTTCATCATGACAAACTTTTGTATCTCTTGGCTCGTGTGTAGCACTTACCAGGGAG 1017
***** ***** ***** ** *** * *****

Mi1.1
Mi1.2
Rpi-blb2
GTATCAACTCTTGTACGTGACTTGGAAAGAGGAACCAAGGAATAAAGAGGGTAATAACCAA 1044
GTATCGACTCTTGTACGTGACTTGGAAAGAGAAATTAAGGAATAAAGAGGGTAATAACCAA 1044
GTATCAACTCTTGTACGCGACTTGGAAAGAGAAATTAAGGATTAAAGAGAGTACTGACGAA 1077
***** ***** ***** ** ***** ***** ** * ** *

Mi1.1
Mi1.2
Rpi-blb2
ACAAATTGTGCAACCCCTAGACTTGTCTGGAAAAATATTGAACTCCTCAAGAAAGATCTCAA 1104
ACAAATTGTGCAACCCCTAGACTTGTCTGGAAAAATATTGAACTCCTCAAGAAAGATCTCAA 1104
ACAAATTGTGCAACCCCTAAAGTTTCTGGAAAAATATTGAACTCCTTAAGGAAGATCTCAA 1137
***** ***** * ** ***** ***** ** *****

Mi1.1
Mi1.2
CATGTTTATCTGAAAGCCCTGGATTCAATCTCAATGTTGCTTCCCCATGAGTATGGACCA 1164
CATGTTTATCTGAAAGCCCCCAATTCAATCTCAATGTTGCTTCCCCATGAGTATGGACCA 1164

Rpi-blb2 CATGTTTATCTGAAAGTCCCGGATTCACTCTCAATATTGCTTCCCCATGAGTGATGGACCT 1197
***** ** *****
Mi1.1 CTCTTCATGCATCTTCTACACATACACTTAAATGATTTGTTAGATTCTAATGCTTATTCA 1224
Mi1.2 CTCTTCATGCATCTTCTACACATGCACCTAAATGATTTGCTAGATTCTAATGCTTATTCA 1224
Rpi-blb2 CTCTTCATGCATCTGCTACAGAGACACTTAGATGATTTGCTGGATTCCCAATGCTTATTCA 1257
***** ** *****
Mi1.1 ATTGCTTTGATAAAGGAAGAAATCGAGCTGGTGAAGCAAGACCTGAAATTCATAAGATCA 1284
Mi1.2 ATTTCTTTGATAAAGGAAGAAATCGAGTTGGTGAGTCAAGAACTGGAAATTCATAAGATCA 1284
Rpi-blb2 ATTGCTTTGATAAAGGAACAAATTTGGCTGGTGAAAGAAAGACTTGGAAATTCATAAGATCT 1317
***** ** *****
Mi1.1 TTCTTTTGTGATGCTG--AGCAAGGATTGTATAAAGATCTCTGGGCACGTGTTCTAGAT 1341
Mi1.2 TTCTTTGGGATGCTGCTGAGCAAGGATTGTATAAAGATATCTGGGCACGTGTTCTAGAT 1344
Rpi-blb2 TTTTTCGCGAATATTG--AGCAAGGATTGTATAAAGATCTCTGGGAACGTGTTCTAGAT 1374
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Mi1.1 GTGGCTTATGAGGCAAAAGATGTATAGATTCAATTATTGTTTCGAGATAAATGGTCTCTTA 1401
Mi1.2 GTGGCTTATGAGGCAAAAGATGTATAGATTCAATTATTGTTTCGAGATAAATGGTCTCTTA 1404
Rpi-blb2 GTGGCATATGAGGCAAAAGATGTATAGATTCAATTATTGTTTCGAGATAAATGGTCTCTTA 1434

Mi1.1 CATCTTATTTTCTCACTTCCCATTACCATAAAGAAGATCAAACTTATCAAAAGAAGAGATC 1461
Mi1.2 CATCTTATTTTCTCACTTCCCATTACCATAAAGAAGATCAAACTTATCAAAAGAAGAGATC 1464
Rpi-blb2 CATCTTATTTTCTCACTTCCCATTACCATAAAGAAGATGATGCTTATCAAAAGAAGAGATC 1494

Mi1.1 TCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGTCTAATCGTTGTGAACCTCTCCCAAG 1521
Mi1.2 TCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGTCTAATCGTTGTGAACCTCTCCCAAG 1524
Rpi-blb2 TCTGATTTACATGAGAACATTTCCAAGAACAGAGGTCTCATCGTTGTGAACCTCTCCCAAG 1554

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Mil.1 AAACCAAGTTGAGAGAAAGTCATTGACAACTGATAAAATAACTGTAGGTTTTGAGGAGGAA 1581

Mil.2 AAACCAAGTTGAGAGAAAGTCATTGACAACTGATAAAATAACTGTAGGTTTTGAGGAGGAG 1584

Rpi-blb2 AAACCAAGTTGAGAGCAAGTCATTGACAACTGATAAAATAACTGTAGGTTTTGAGGAGGAG 1614

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Mil.1 ACAAACTTGATACTTAGAAAGCTCACCAAGTGGATCGGCAGATCTAGATGTCAATTCGATC 1641

Mil.2 ACAAACTTGATACTTAGAAAGCTCACCAAGTGGACCCGCAGATTTAGATGTCAATTCGATC 1644

Rpi-blb2 ACAAACTTGATACTTAGAAAGCTCACCAAGTGGACCCGCAGATCTAGATGTCAATTCGATC 1674

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Mil.1 ACTGGTATGCCGGGTTTCAGGTAAATACTACTTTGGCATACAAAGTATACAATGATAAGTCA 1701

Mil.2 ACCGGTATGCCGGGTTTCAGGTAAATACTACTTTGGCATACAAAGTATACAATGATAAGTCA 1704

Rpi-blb2 ATTGGTATGCCGGGTTTAGGTAAATACTACTTTGGCGTACAAAGTATACAATGATAAAATCA 1734

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Mil.1 GTTTCCTAGCCGTTTCGACCTTCGTGCAATGGTGCA CGGTCGACCAAGGATGTGATGAGAAG 1761

Mil.2 GTTTCCTAGACATTTTTCGACCTTCGTGCAATGGTGCA CGGTCGATCAAGGATATGACGACAAG 1764

Rpi-blb2 GTTTCCTAGCCATTTTCGACCTTCGTGCAATGGTGCA CGGTCGACCAAGTATATGACGAGAAG 1794

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Mil.1 AAGTTGTTGAATACAATTTTCAGTCAAGTTAGTGACTCAGATTCAAAATTGAGTGAGAAT 1821

Mil.2 AAGTTGTTGGATACAATTTTCAGTCAAGTTAGTGACTCAGATTCAAAATTGAGTGAGAAT 1824

Rpi-blb2 AAGTTGTTGGATAAAATTTTCAATCAAGTTAGTGACTCAAAATTCAAAATTGAGTGAGAAT 1854

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Mil.1 ATTGATGTTGCTGATAAATTACGGAAACAACACTGTTTGGAAAAGAGGTATCTTATTGTCTTA 1881

Mil.2 ATTGATGTTGCTGATAAATTGCGGAAACAACACTGTTTGGAAAAGAGGTATCTTATTGTCTTA 1884

Rpi-blb2 ATTGATGTTGCTGATAAACTACGGAAACAATTTGTTTGGAAAAGAGGTATCTTATTGTCTTA 1914

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Replacement Sheets

Mi1.1
GATGACGTGTGGGATACTACTACATGGGATGAGTTAACAGACCTTTTCCTGAATCTAAG 1941

Mi1.2
GATGATGTGGGATACTACTACATTGGATGAGTTGACAAGACCTTTTCTGAAGCTAAG 1944

Rpi-blb2
GATGACGTGTGGGATACTAAATACATGGGATGAGCTAACACAGACCTTTTCTGATGGTATG 1974

[illegible]

Mi1.1
AAAGGAAGTAGGATTATTTTGACAACTCGGAAAAGGAAGTGGCTTTGCATGGAAAGCTG 2001

Mi1.2
AAAGGAAGTAGGATTATTTTGACAACTCGAGAAAAGGAAGTGGCTTTGCATGGAAAGCTG 2004

Rpi-blb2
AAAGGAAGTAGAATTATTTGACCACTCGAGAAAAGAAAGTTGCTTTGCATGGAAAGCTC 2034

Mi1.1
AACACTGATCCTCTTGACCTTCGATTGCTAAGACCAGATGAAAGTTGGGAACCTATTAGAG 2061

Mi1.2
AACACTGATCCTCTTGACCTTCGATTGCTAAGACCAGATGAAAGTTGGAACTTTTAGAT 2064

Rpi-blb2
TACACTGATCCTCTTAACCTTCGATTGCTAAGATCAGAAGAAAGTTGGGAGTTATTAGAG 2094

[illegible]

Mi1.1
 AAAAGGCCATTTGGGAATGAGAGTTGCCCTGATGAACTATTAGATGTCGGTAAAGAAATA 2121

Mi1.2
AAAAGGACATTTGGTAATGAGAGTTGCCCTGATGAACTATTAGATGTCGGTAAAGAAATA 2124

Rpi-blb2
AAAAGGGCATTTGGAAACGAGAGTTGCCCTGATGAACTATTGGATGTTGGTAAAGAAATA 2154

[illegible]

Mi1.1
GCCGAAAATTGTAAAGGGCTTCCTTTGGTGGCTGATCTGATTGCTGGAGTCATTGCTGGG 2181

Mi1.2
GCCGAAAATTGTAAAGGGCTTCCTTTGGTGGCTGATCTGATTGGAGTCATTGCTGGG 2184

Rpi-blb2
GCCGAAAATTGTAAAGGGCTTCCTTTGGTGGTGGATCTGATTGCTGGAATCATTTGCTGGG 2214

Mi1.1
AGGAAAGAAAGGAGTGTGGCTTGAAGTTCAAAGTAGTTGAGTCTTTATTG 2241

Mi1.2
AGGAAAGAAAGGAGTGTGTGGCTTGAAGTTCAAAGTAGTTGAGTTCTTTATTTTG 2244

Rpi-blb2
AGGGAAGAAAGAGTGTGGCTTGAAGTTGTAAATAATTGCATTCCTTTATTG 2274

Mil.1.1 AACAGTGAAGTGGAGTGATGAAAGTTATAGAATTAAAGTTATGACCATTTACCACATCAC 2301
Mil.1.2 AACAGTGAAGTGGAGTGATGAAAGTTATAGAATTAAAGTTATGACCATTTACCACATCAC 2304
Rpi-blb2 AAGAAATGAAGTGGAGTGATGAAAGTTATAGAATAAAGTTATGACCACTTACCTGATCAC 2334
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Mil.1.1 CTCGAAGCCATGCTTGCTGTATTTTGCAAGTTTTCCGAAGGACACTTCATTGACAATCTAT 2361
Mil.1.2 CTCGAAGCCATGCTTGCTTCACTTTTGCAAGTTGGCCGAAGGACACTCCTTTGACAATCTAT 2364
Rpi-blb2 CTGAAGCCATGCTTGCTGTACTTTTGCAAGTGCGCCGAAGGACTGGGTAACGACAATCCAT 2394
** * ***** ** * ***** ** * ***** ** * ***** ** * *****

Mil.1.1 GAGTTGAATGTTTATTTTCGGTGTGAAGGATTTGTGGGAAAGACGGAGATGAACAGTATG 2421
Mil.1.2 TTGTTTACTGTTTATTTTGGGTGCTGAAGGATTTGTGGAAAAAGACGGAGATGAAGGGTATA 2424
Rpi-blb2 GAGTTGAAACTTATTTTGGGGTTTGAAGGATTTGTGGAAAAAGACAGATATGAAGAGTCTG 2454
*** * ** ** * ***** ** * ***** ** * ***** ** * *****

Mil.1.1 GAAGAAGTGGTGAAGATTTATATGGATGATTTAAATTTACAGTAGCTTGGTAAATTTGTTTC 2481
Mil.1.2 GAAGAAGTGGTGAAGATTTATATGGATGATTTAAATTTCCAGTAGCTTGGTAAATTTGTTTC 2484
Rpi-blb2 GAAGAAGTGGTGAAGATTTATTTGGATGATTTAAATTTCCAGTAGCTTGGTAAATTTGTTTC 2514
***** ** * ***** ** * ***** ** * ***** ** * *****

Mil.1.1 AATGAGATAGGTTATGCACCTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTGTTG 2541
Mil.1.2 AATGAGATAGGTTATGATATACTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTGTTG 2544
Rpi-blb2 AATGAGATAGGTTATACCCCTACTTGCCAACTTCATGATCTTGTGCATGACTTTTGTGTTG 2574
***** ** * ***** ** * ***** ** * ***** ** * *****

Mil.1.1 ATAAAAGCAAGAAAGGAAAAATTTGTTTGATCAGATAAGATCAAGTGCTCCATCAGATTG 2601
Mil.1.2 ATAAAAGCAAGAAAGGAAAAATTTGTTTGATCGGATAAGATCAAGTGCTCCATCAGATTG 2604
Rpi-blb2 ATAAAAGCAAGAAAGGAAAAAGTTGTGTGATCGGATAAGTTCAAGTGCTCCATCAGATTG 2634
***** ** * ***** ** * ***** ** * ***** ** * *****

Mil.1.1 TTGCCTCGTCAAATTACCATTGATTGTGATGAGGAGGAG-- --CACTTTGGGCTTAATTT 2658

Mi1.2
Rpi-blb2
TTGCCCTCGTCAAATTACCATTTGATTATGATGAGGAGGAGCACCTTTGGGCTTAATTTT 2664
TTGCCACGTCAAATTAGCATTTGATTATGATGATGATGAAGAGCACCTTTGGGCTTAATTTT 2694

Mi1.1
Mi1.2
Rpi-blb2
GTCATGTTTCGATTCAAATAAGAAAAGGCATTCTGGTAAACACCTCTATTCTTTGAGGATA 2718
GTCATGTTTCGATTCAAATAAGAAAAGGCATTCTGGTAAACACCTCTATTCTTTGAGGATA 2724
GTCCCTGTTTCGGTTCAAATAAGAAAAGGCATTCCGGTAAACACCTCTATTCTTTGACCATA 2754

Mi1.1
Mi1.2
Rpi-blb2
ATTGGAGACCACTGGATGACAGTGTTTCTGATGCATTTTCACTAAGACACTTTGAGGCTT 2778
AATGGAGACCACTGGATGACAGTGTTTCTGATGCATTTTCACTAAGACACTTTGAGGCTT 2784
AATGGAGATGAGCTGGACGACCATCTTTCTGATACATTTTCACTAAGACACTTTGAGGCTT 2814

Mi1.1
Mi1.2
Rpi-blb2
CTTAGAGTGTGGACCTGCATACGTCTTTTATCATGGTGAAAGATTCTTTGCTGAATGAA 2838
ATTAGAGTGTGGACCTGGAAACCTCTTTTAATCATGGTGAATGATTCTTTGCTGAATGAA 2844
CTTAGAACCTTGCAACCTGGAATCCTCTTTTATCATGGTTAAAGATTCTTTGCTGAATGAA 2874

Mi1.1
Mi1.2
Rpi-blb2
ATATGCATGTTGAATCATTTGAGGTACTTATCCATTGACACACAAGTTAAATATCTGCCT 2898
ATATGCATGTTGAATCATTTGAGGTACTTAAAGAAATTCGGACACAAGTTAAATATCTGCCT 2904
ATATGCATGTTGAATCATTTGAGGTACTTAAAGCAATTTGGGACAGAAGTTAAATCTCTGCCT 2934

Mi1.1
Mi1.2
Rpi-blb2
TTGTCTTTCTCAAACCTCTGGAATCTAGAAAAGCCTGTTTGTGTCTACCAACAGATCAATC 2958
TTCTCTTTCTCAAACCTCTGGAATCTAGAAAAGCTGTGTTGTGTCTAAACAAGGATCAATC 2964
TTGTCTTTCTCAAACCTCTGGAATCTAGAAAATCTTGTGTTGTGATAACAAGAATCAACC 2994

Mi1.1
Mi1.2
TTGGTACTATTACCGAGAATTTTGGATCTTGTAAAGTTGCGAGTGCTGTCCGTGGATGCT 3018
TTGGTACTATTACCGAGAATTTTGGATCTTGTAAAGTTGCGAGTGCTGTCCGTGGTGCT 3024

Rpi-blb2 TTGATACTATTACCGAGAAATTTGGGATCTTTGTAAAGTTGCAAGTGTCTGTTCACGACTGCT 3054
*** *****

Mi1.1 TGTTCCTTTCTTTGATATGGATGCAGATGAATCAATATTGATAGCAGAGGACACAAAAGTTA 3078
Mi1.2 TGTTCCTTTCTTTGATATGGATGCAGATGAATCAATATTGATAGCAAAAGGACACAAAAGTTA 3084
Rpi-blb2 TGTTCCTTTCTTTGATATGGATGCAGATGAATCAATATTGATAGCAGAGGACACAAAAGTTA 3114

Mi1.1 GAGAACTTGAGAAATATTAAACGGAACTGTTGATTTCCCTATTTCGAAAGATACAAAGAATATT 3138
Mi1.2 GAGAACTTGAGAAATATTAGGGGAACTGTTGATTTCCCTATTTCGAAAGATACAAATGAATATT 3144
Rpi-blb2 GAGAACTTGACAGCAATTAGGGGAACTCGTGTCTTTCCCTATTTGAAAGATACAGAGGATATT 3174

Mi1.1 TTCAAAAGGTTTCCCAATCTTCAGTTGCTTTTCATTTTGAACTCAAGGAGTCATGGGATTAT 3198
Mi1.2 TTCAAAAGGTTTCCCAATCTTCAGGTGCTTCAGTTTGAACTCAAGGAGTCATGGGATTAT 3204
Rpi-blb2 TTCAAAAGGCTTCCCAATCTTCAAGTGTCTTCATTTCAAACCTCAAGGAGTCATGGGATTAT 3234

Mi1.1 TCAACAGAGCAACATTGGTTCTCGGAATTGGATTTCCCTAACTGAAC TAGAAACACTCTCT 3258
Mi1.2 TCAACAGAGCAACATTGGTTCCCGAAATTGGATTTGCCCTAACTGAAC TAGAAACACTCTGT 3264
Rpi-blb2 TCAACAGAGCAATATTGGTTCCCGAAATTGGATTTCCCTAACTGAAC TAGAAACACTCACT 3294

Mi1.1 GTAGGTTTTAAAGTTCAAACACAAACGATAGTGGTCCCTCTGTAGCGGACAAATCGGCCG 3318
Mi1.2 GTAGGTTTTAAAGTTCAAACACAAACCACTGTGGTCCCTCTGTGTGACAAATCGGCCG 3324
Rpi-blb2 GTAGATTTTGAAGATCAAACACAAATGACAGTGGTCCCTCTGCAGCCATAAAATCGGCCA 3354

Mi1.1 TGGGATTTTCACTTCCCTTCAAATTTGAAAAATACTGTGGTTGCGTGAAATTTCCGCTGACA 3378
Mi1.2 TGGGATTTTCACTTCCCTTCAAATTTGAAAGAACTGTGTGTGATGACTTTTCCTCTGACA 3384
Rpi-blb2 TGGGATTTTCACTTCCCTTCGAGTTTGAAAAGATTGCAATTGCAATGAATTTCTCTGACA 3414

Mi1.1 TCCGATTCACTATCAACAATAGCGAGACTGCCCAACCTTGAAAGAGTTGTCCCTTTATCAT 3438
Mi1.2 TCCGATTCACTATCAACAATAGCGAGACTGCCCAACCTTGAAAAATTTGTCCCTTTATGAT 3444
Rpi-blb2 TCCGATTCACTATCAACAATAGCGAGACTGCTGAACCTTGAAAGAGTTGTACCTTTATCGT 3474

Mi1.1 ACAATCATCCATGGAGAAGAAATGGAACATGGGGAGGAAGACACCTTTGAGAAATCTCAA 3498
Mi1.2 ACAATCATCCAGGAGAGAAGAAATGGAACATGGGGAGGAAGACACCTTTGAGAAATCTCAA 3504
Rpi-blb2 ACAATCATCCATGGGGAAGAAATGGAACATGGGAGGAAGAAAGACACCTTTGAGAAATCTCAA 3534

Mi1.1 TTTTGTGAACCTTCAATCAAGTTAGTATTTCCAAAGTGGGAGGTTGGAGAGGAATCCTTCCCC 3558
Mi1.2 TTTTGTGAACCTTGGTCTACTGACTCTTTCAAAGTGGGAGGTTGGAGAGGAATCCTTCCCC 3564
Rpi-blb2 TGTGTGATGTTGAGTCAAGTGATCTTTCAAAGTGGGAGGTTGGAGAGGAATCCTTTTCCC 3594

Mi1.1 AATCTTGAGAAATTAAAACTGCGGGGATGTCTATAAGCTAGAGGAGATTCCACCTAGTTT 3618
Mi1.2 AATCTTGAGAAATTAAAACTGCAGGAATGTGTAAGCTTGAGGAGATTCCACCTAGTTT 3624
Rpi-blb2 ACGCTTGAGAAATTAGAACTGTCGACTGTCTATAATCTTGAGGAGATTCCGCTAGTTT 3654

Mi1.1 GGAGATATTTATTCATTGAAATCTATCAAAATTTGTAAGAGTCCTCAACTTGAAGATTCT 3678
Mi1.2 GGAGATATTTATTCATTGAAATTTATCAAAATTTGTAAGAGTCCTCAACTTGAAGATTCT 3684
Rpi-blb2 GGGATATTTATTCCTTGAAAAATTATCGAACTTGTAAGGAGCCCTCAACTTGAAAAATCC 3714

Mi1.1 GCTCTCAAAATTAAGGAATACGCTGAAGATATGAGGGGAGGGACGAGCTTCAGATCCTT 3738
Mi1.2 GCTCTCAAGATTAAGAAATACGCTGAAGATATGAGAGGAGGGAACGATCTTCAGATCCTT 3744
Rpi-blb2 GCTCTCAAGATTAAGGAATATGCTGAAGATATGAGGGGAGGGACGAGCTTCAGATCCTT 3774

Mi1.1 GGCCAAAAGAATATCCCCCTTATTTAAGTAG 3768
Mi1.2 GGCCAGAAGAATATCCCCCTTATTTAAGTAG 3774
Rpi-blb2 GGCCAGAAGGATATCCCGTTATTTAAGTAG 3804
